

1 GCCACCAACGATCTAGCTTCAAATTAATGTTGCCCTAGTGGTAAAGGACAGAGACCCCTCAGACTGATGAAATGGGCTCAGAATTACTTAGACAA  
 37 AGCGGATATTTGCCACTCTCTTCCCTTTTCTGTGTTTTTCTAGTGAAGAGACCTGAAAGAAAAAGTAGGGAGAACATAATGAGAACAATAACG  
 193 GTAACTCTTTCATTGTCTAGTTCAGTGCTGGACTTGGGACTTAGGAGGGGCAATGGAGCCGCTTAGTGCCTACATCTGACTTGGACTGAAATATA  
 289 CGTCAGAGACAAGATTGTCTCATATCCGGGGAAATCATACCTATGACTAGGACCGGAAGAGGAAGCACTGCCTTTACTTCAGTGGGAATCTCGGC  
 385 CTCAGCCTGCAAGCCAAAGTGTTCACTGAGAAAAGCAAGAGAATAAGCTAATACTCTGTCTCTGAACAAAGGCAGCGGCTCTTGGTAAAGCTACT  
 481 CCTTGATCGATCCTTTGCACCGGATTGTCAAAGTGGACCCCAAGGGGAGAGTGGAGCAAGAACTTACCACCAAGCACTCCAAGAGGCCAGAA  
 577 GCAAACCTGGAGGTTGAGACCCAAAGAAAGCTGGAAACATGCTGACTTTGTACACTGTGAGGACACAGAGTCTGTTCTCGAAAGCCAGTGTCAAC  
 LEVRPKESWNHADFVHCEDTESVPGKPSVN 30  
 673 GCAGATGAGGAAGTGGAGCTCCCAAATCTGCGGTGTATGTGGGCAAGGCCACTGGCTATCACTTCAATGTCATGACATGTGAAGGATGCAAG  
 ADEEVGCPQICRVCGDKATGYEFNVMTCEGCK 62  
 769 GGCTTTTTCAGGAGGGCCATCAAACGCAAGCCCGGCTGAGGTGCCCTTCCGGGAAGGGCGCTGGAGATCACCCGGAAGACCCGGGCGGACGTCC  
 GFFRRAWKRLRCLRCFPRKGAACEITRKRQC 94  
 865 CAGGCTCTCCCGCTGCGCAAGTGCCTGGAGAGCGGCATGAAGAAGGAGATGATCATGTCCGACGAGCCGCTGGAGGAGAGCGGGCTTGTATCAAG  
 QACRLRKCLZSGMKKKEHIMSD EAV EERRALIK 126  
 961 CGGAAGAAAAGTCAACCGACAGGGAAGTCAAGCACTGGGAGTGCAGGGGCTGACAGAGCAGCAGCCGATGATGATCAGGGAGCTGATGGACGCTCAG  
 RKKSERTGTQPLGVQGLTEEQRMHIRELEMDAQ 158  
 1057 ATGAAAACCTTTGACACTACCTTCTCCCATTTCAAGAATTTCCGGCTGCCAGGGGTGCTTAGCAGTGGCTGGAGTGGCAGAGCCTCTGCAGGCC  
 MKTFDTTFSSHFKNFRLLPGVLS SGC ELP EPLQA 190  
 1153 CCATCGAGGGAAGAAGCTGCCAAGTGGAGCCAGGTCCGGAAAGATCTGTCTTTGAAGGTCTCTCTGCAAGCTGCGGGGGAGGATGCCAGTGT  
 PSREEEAAKWSQVVRKDLCSLKVSLQAAGGGGWQC 222  
 1249 CTGGAATAACAACNCCAGCCGACAGTGGCGGAAGAGATCTTCTCCCTGCTGCCCCACATGGCTGACATGTCAACCTACATGTTCAAGGCATC  
 LELQTTPSRQWRKEIFSLPLPHHAD MSTYMF KGI 256  
 1345 ATCAGCTTTGCCAAAGTCACTCTCTACTTCAGGGAGTTCGCCATCGAGGACCAGATCTCCCTGCTGAAGGGGGCCGCTTTCGAGCTGTGTCACTG  
 ISPAKVZSYFRDLPIEDQISLLKGA AFELCQL 286  
 1441 AGATTCAACACAGTGTTCACCGCGGAGACTGGAACCTGGGAGTGTGGCCGGCTGTCTACTGCTTGGAGACACTGCAGGTGGCTTCCAGCAACTT  
 RFNTVFNAETGTWECGRLSYCLEDTAGGFQQL 318  
 1537 CTACTGGAGCCCATGCTGAAATCCACTACATGCTGAAGAAGCTGCAGCTGCATGAGGAGGAGTATGTGCTGATGCAGGCCATCTCCCTCTTCTCC  
 LLEPHMLKFHYMLKKLLQLHEEEYVLMQAISLFS 350  
 1633 CCAGACTGCCAGGTCTCTGTCAGCACCGCGTGGTGGACCAGCTGCAGGAGCAATTCGCCATTACTCTGAAGTCTACATTGAATGCAATCGGGCCC  
 PDRP.GV.LQH RVVDQLQE QPAITLKS YTECNR P 382  
 1729 CAGCCTGCTCATAGGTTCTGTCTCTGAAGATCATGGCTACTCACCAGGCTCCGCAAGCATCAATGCTCAGCACACCCAGCGGCTGCTGGGCATC  
 QPAHRFLFLKIMAHLT E LRSINAQH TQRLRI 414  
 1825 CAGGACATACACCCCTTTGCTACGCCCTCATGCAGGAGTGTTCGGCATCAGGTAGCTGAGCGGCTGCCTTGGGTGACACCTTCGAGAGGCAG  
 QDIHFFATPLMQELFGITGS 436  
 1921 CCAGACCCAGAGCCCTCTGAGCCGGCACTCCCGGGCAAGACAGATGGACACTGCCAAGAGCCGACAATGCCCTGCTGGCTGTCTCCCTAGGGAA  
 2017 TTCTGCTATGACAGCTGGCTAGCATCTCTCAGGAAGGACATGGGGTGCCTC 2068

FIG. 1A



09340008, 042001

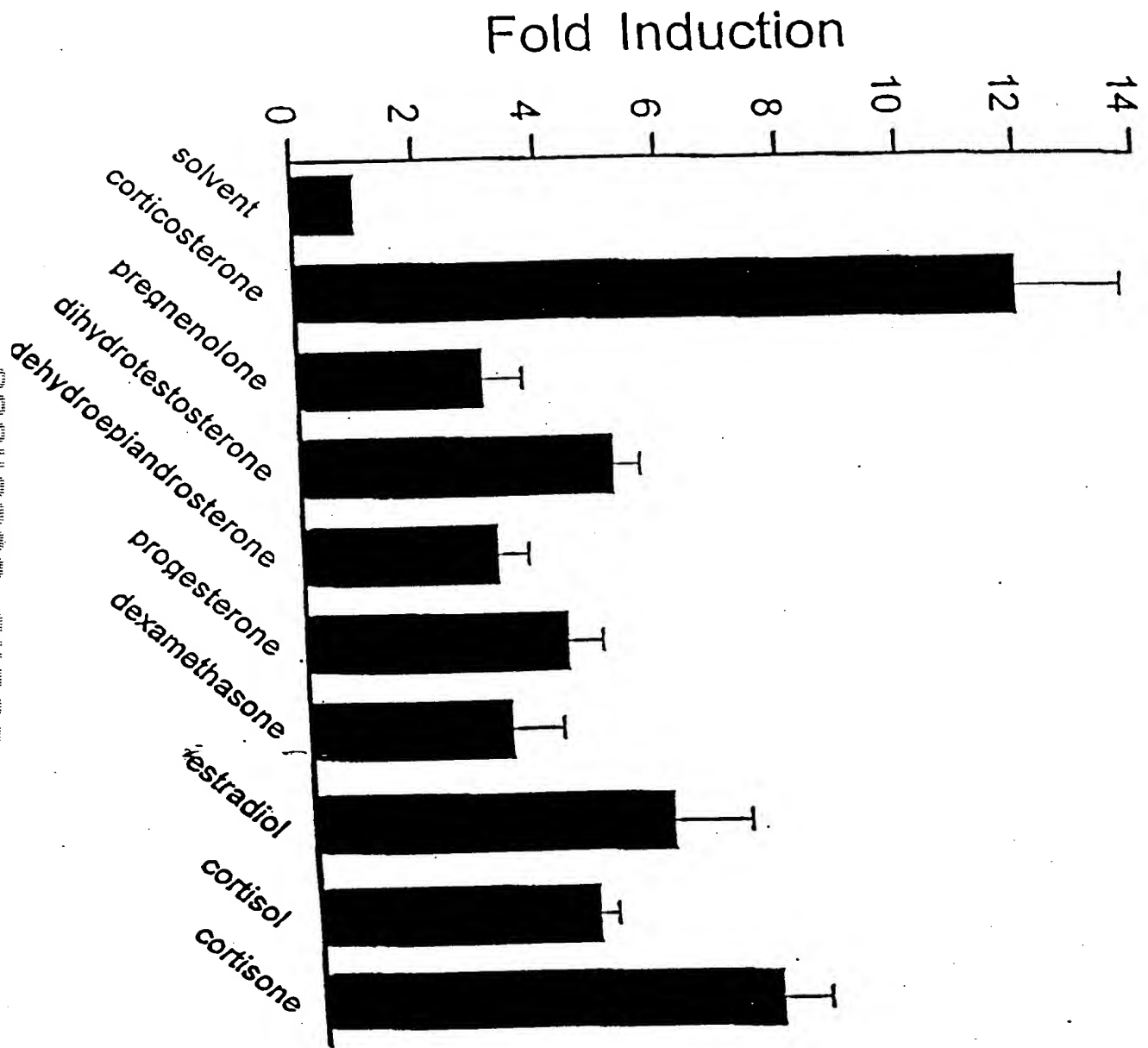


FIG. 2

09640008 . 042001

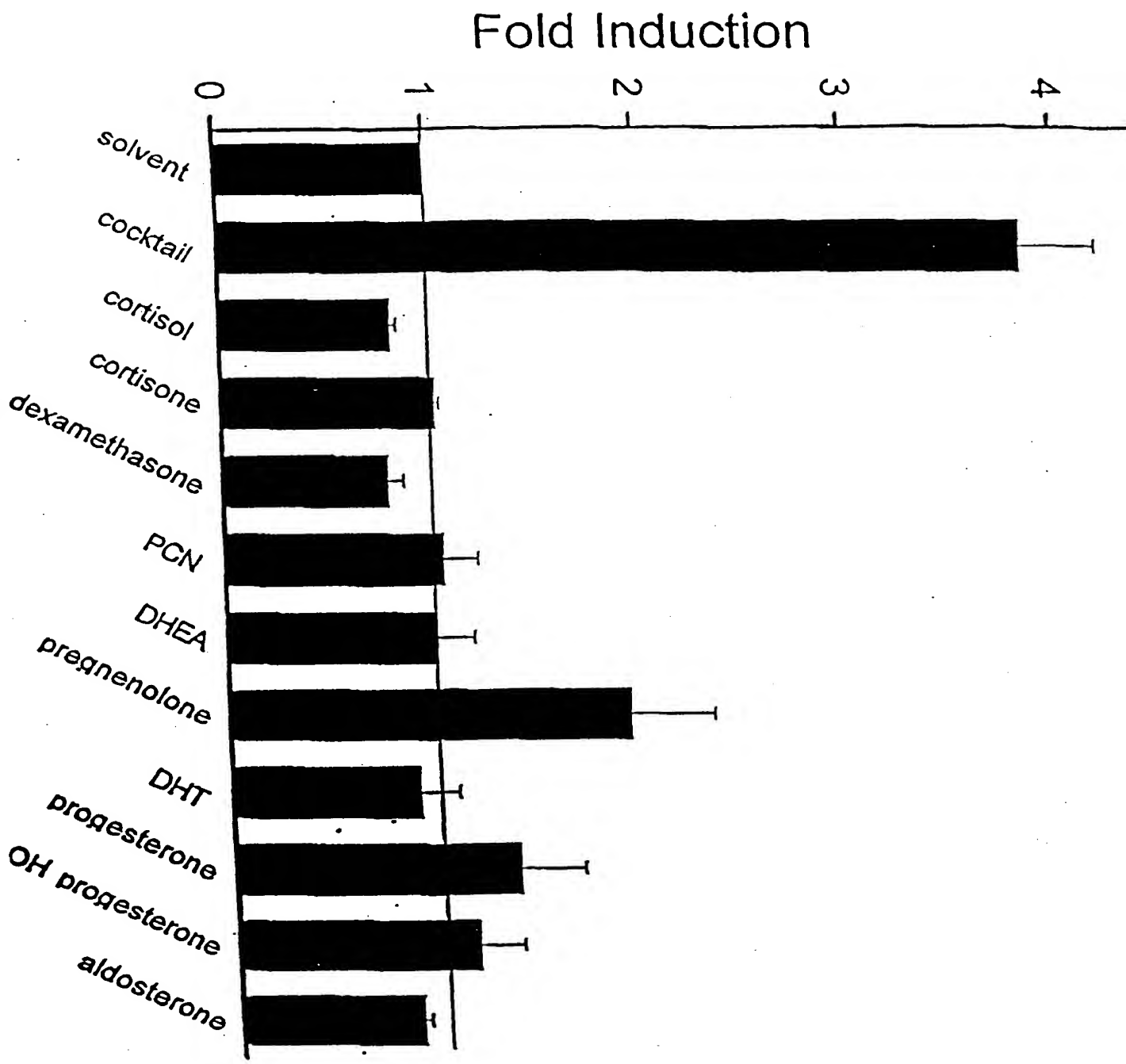


FIG. 3

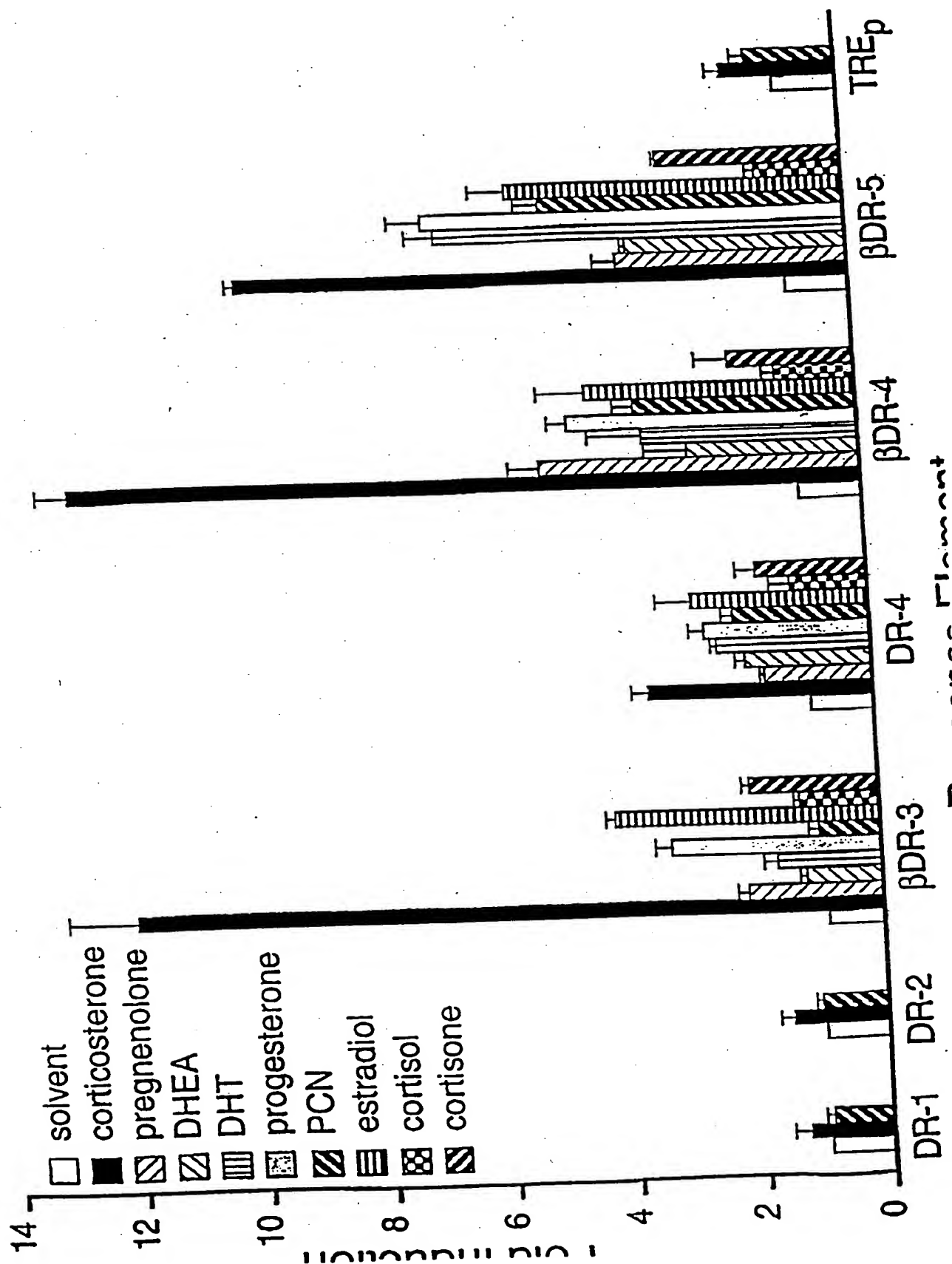


FIG. 4

1002490 2004060

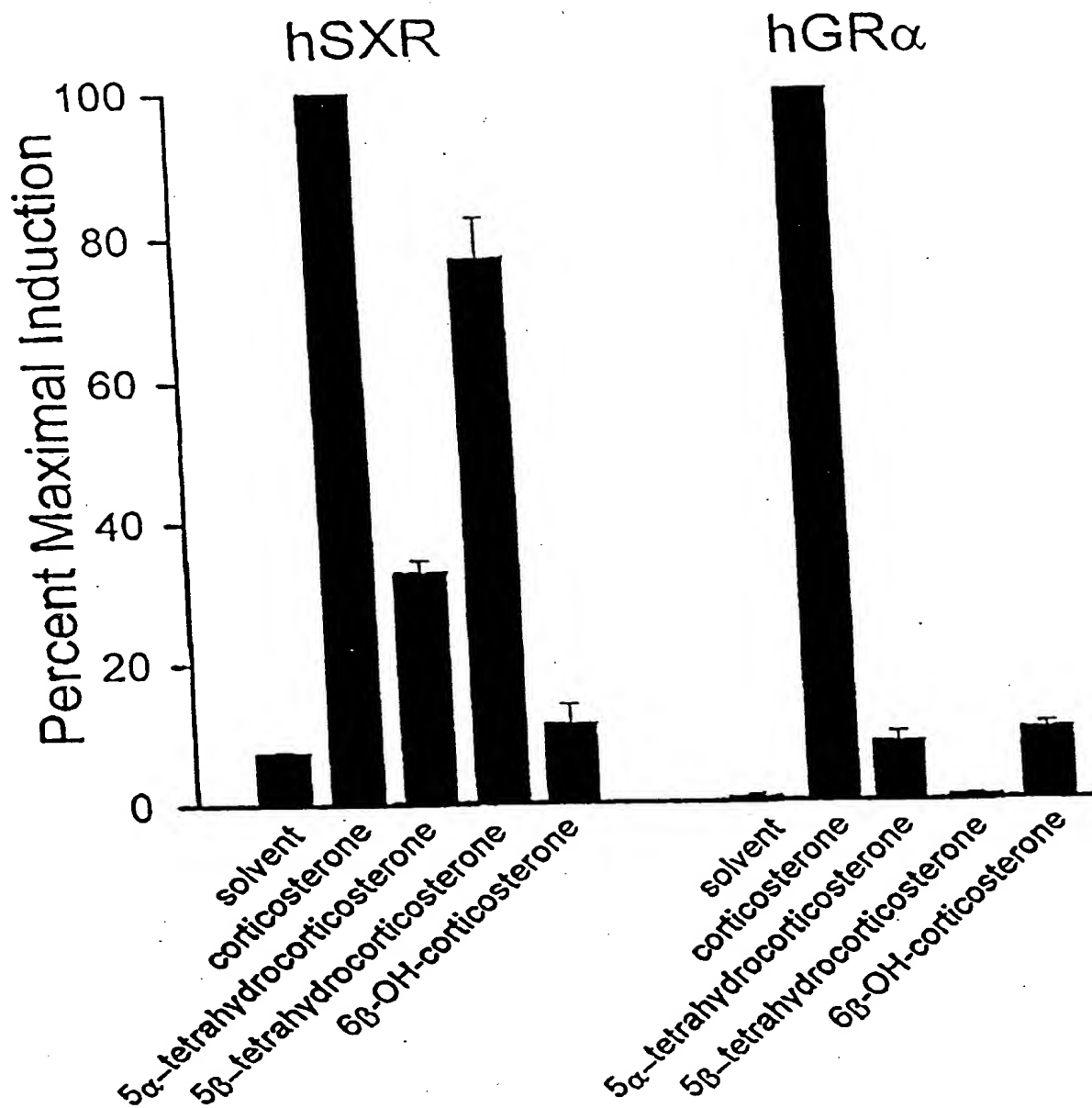


FIG. 5

DR-3

rCYP3A1  
rCYP3A2  
rUGT1A6

tagac AGTTCA tga AGTTCA tctac  
taagc AGTTCA taa AGTTCA tctac  
actgt AGTTCA taa AGTTCA catgg

DR-4

rbCYP2C1  
rP450R

caatc AGTTCA acag GGTTCa ccaat  
cac AGGTGA gctg AGGCCA gcagc AGGTCTG aaa

DR-5

rCYP2A1  
rCYP2A2  
rCYP2C6  
hCYP2E1

gtgca GGTTCa actgg AGGTCA acatg  
gtgct GGTTCa actgg AGGTCA gtatg  
agtct AGTTCA gtggg GGTTCa gtctt  
gagat GGTTCa aggaa GGGTCA ttaac

FIG. 6A

CYP3A4  
CYP3A5  
CYP3A7

tagaata TGAACT caaagg AGGTCA gtgagtgg  
tagaata TGAACT caaagg AGGTAA gcaaaggg  
tagaata TTA ACT caatgg AGGC.A gtgagtgg

FIG. 6B

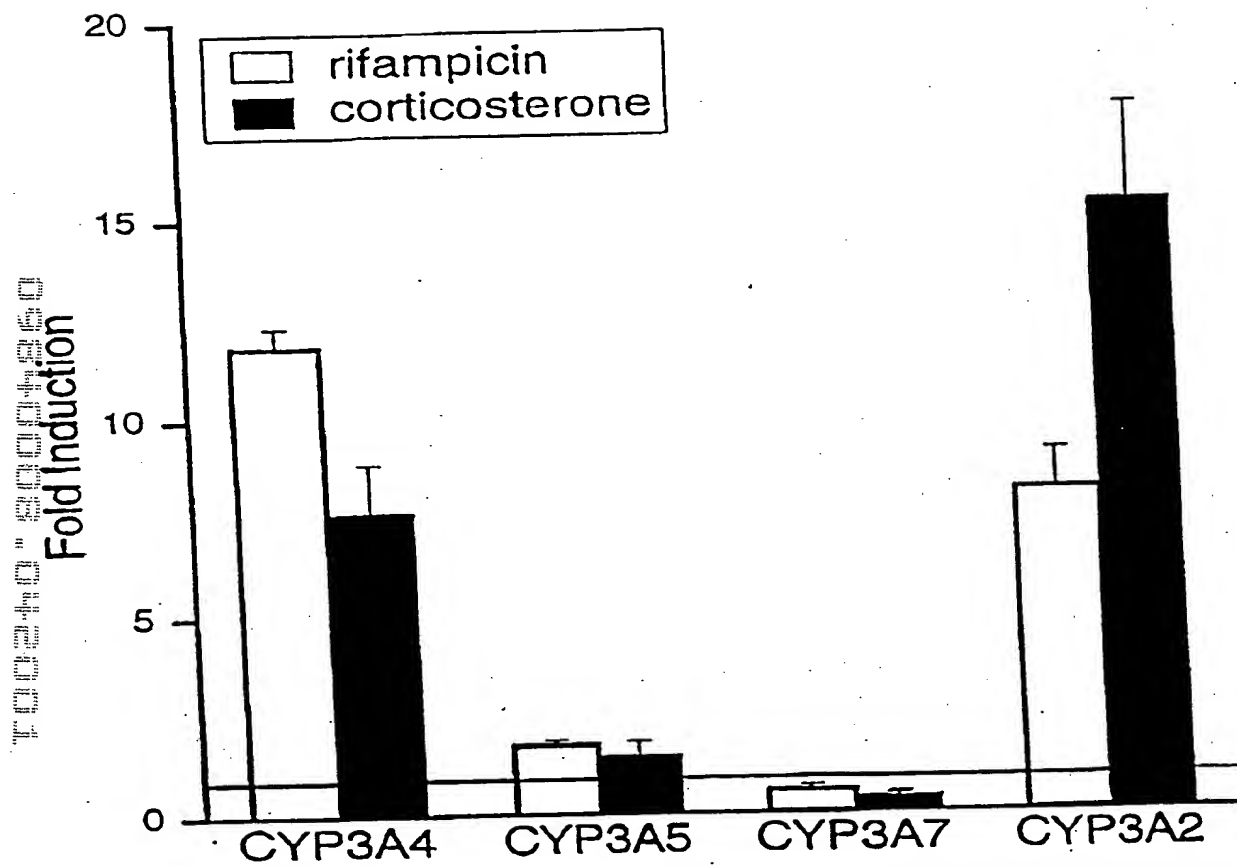
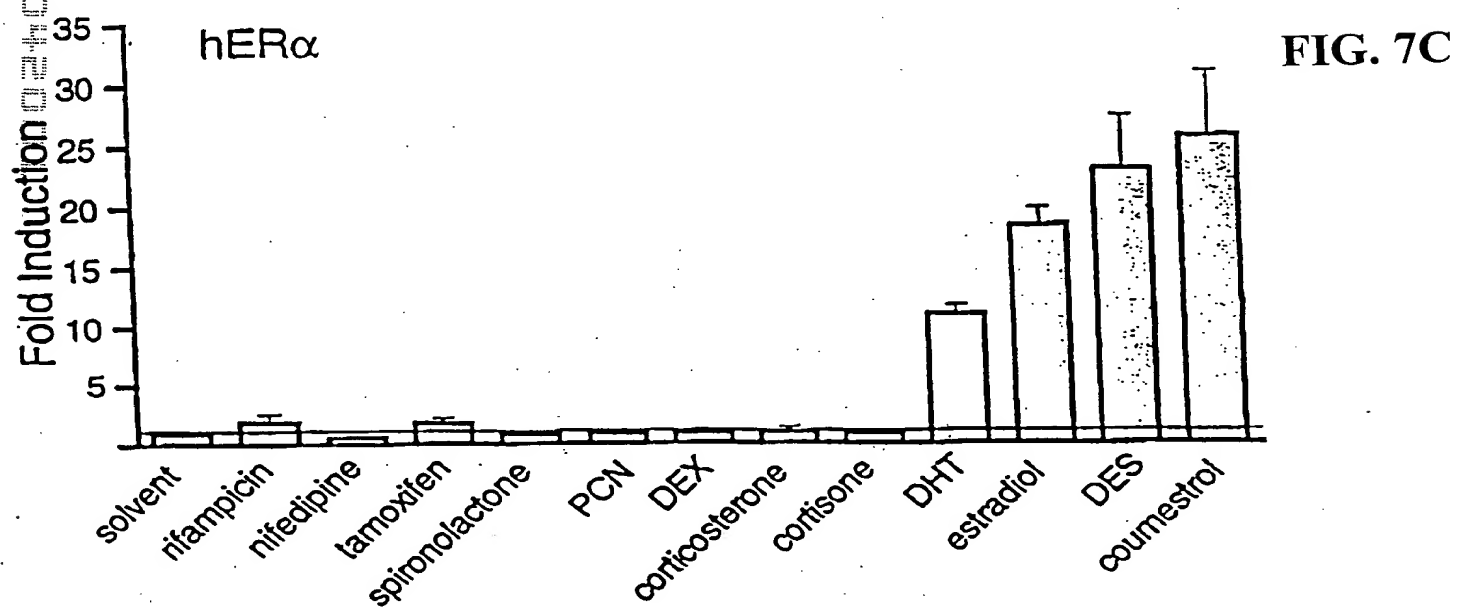
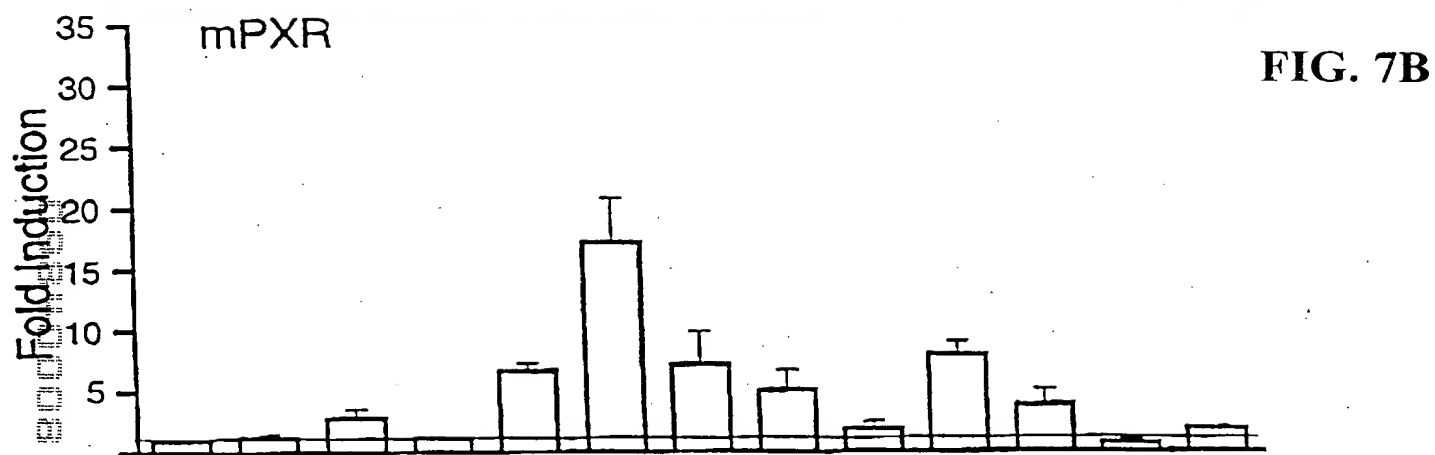
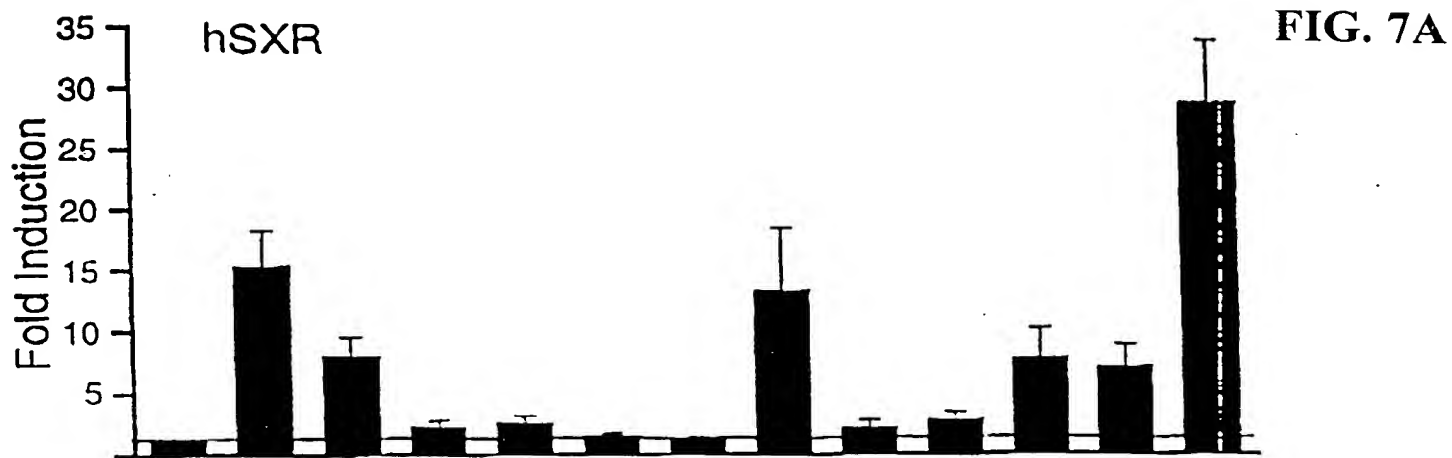
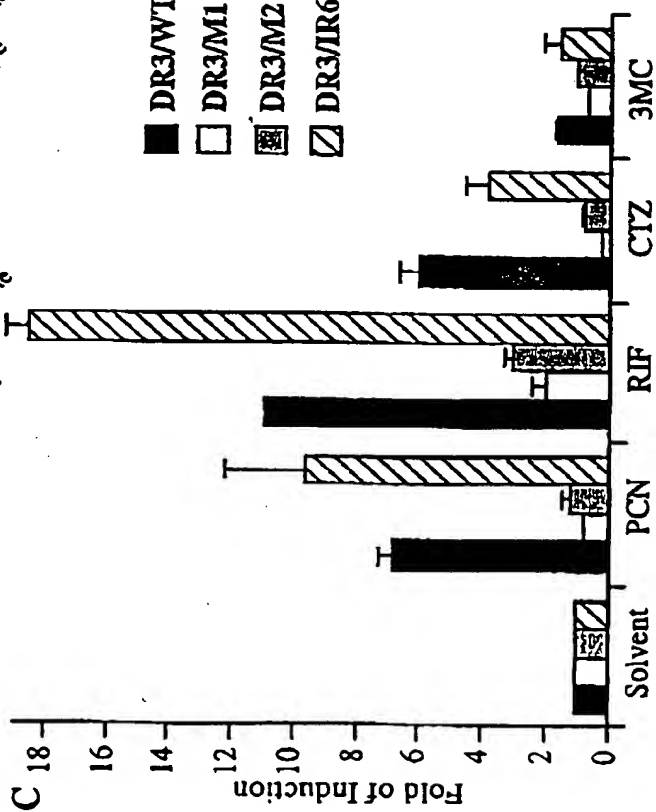
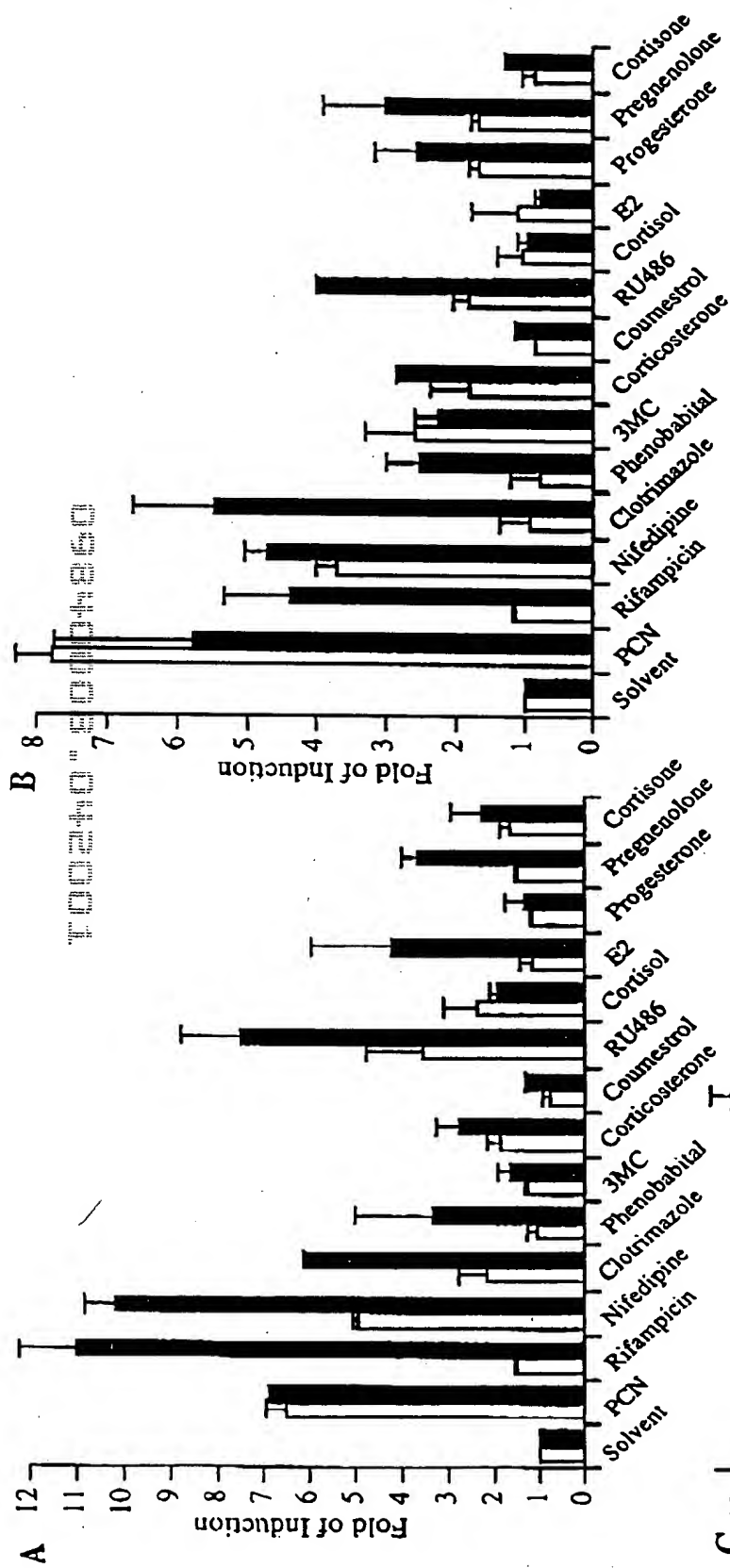


FIG. 6C







DR3/WT (TGAACCTcaTGAACT)  
 DR3/M1 (TGTTCCTcaTGTTCCT)  
 DR3/M2 (ACAACTcaTGAACT)  
 DR3/IR6 (TGAACCTcaaggAGGTCA)

**FIG. 8**

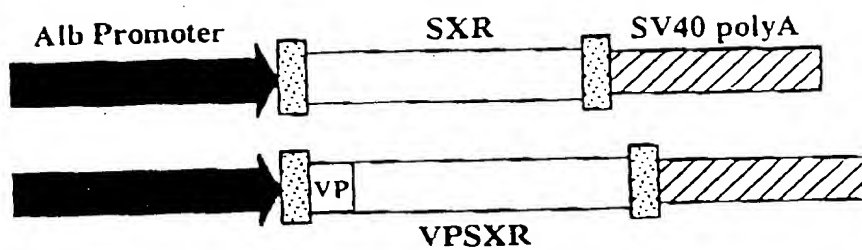


FIG. 9

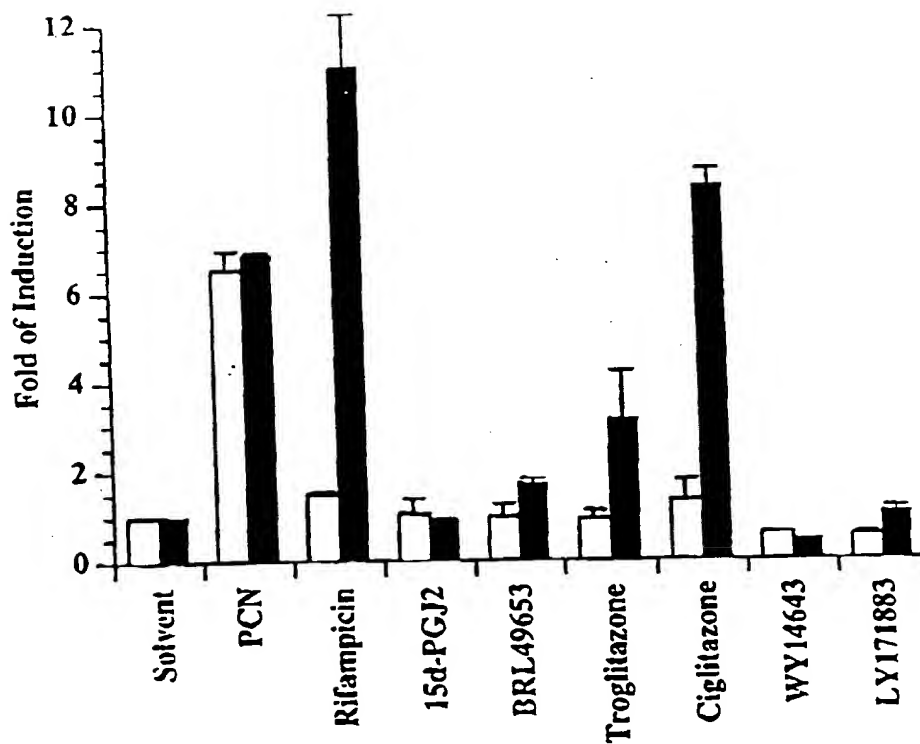


FIG. 10

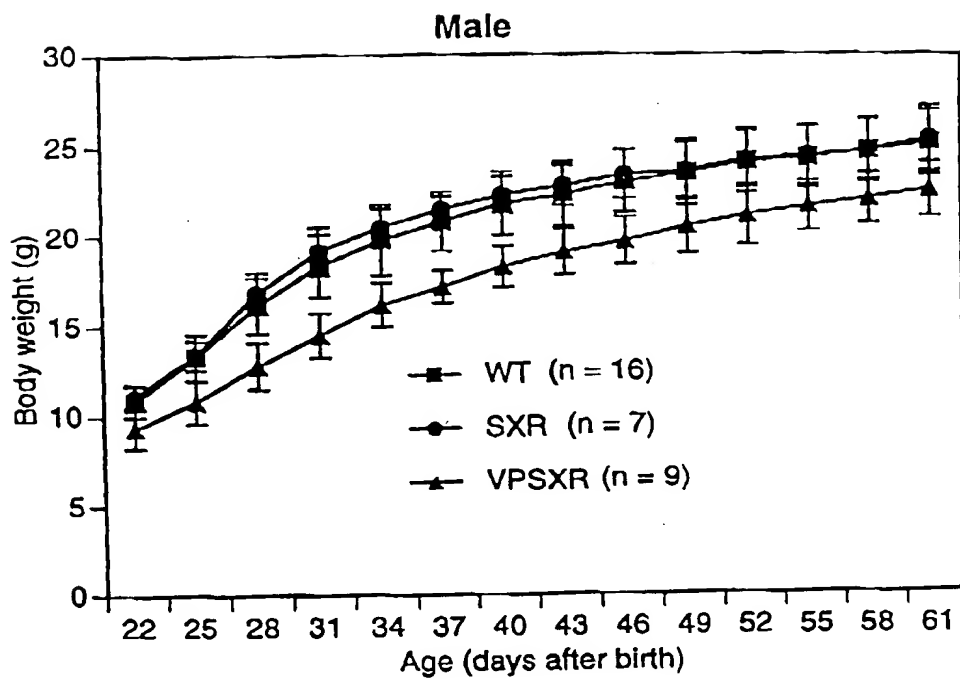


FIG. 11

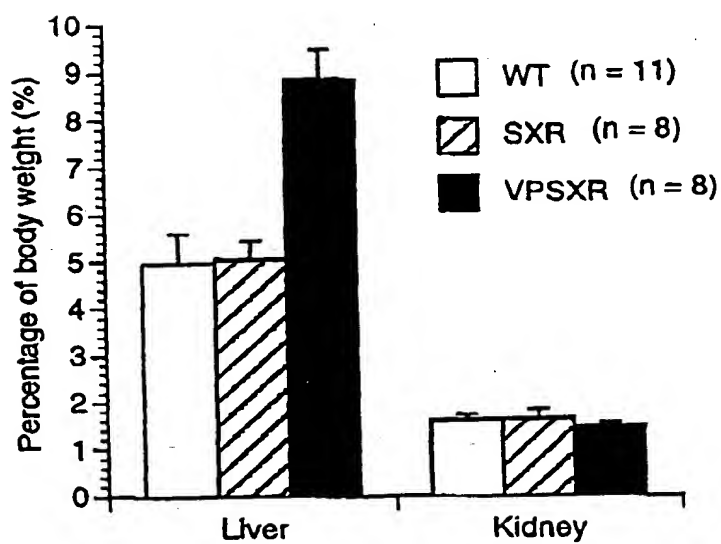


FIG. 12